

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,375

DATE: 05/12/2000
TIME: 14:24:30

INPUT SET: S35473.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: ARTHUR, MICHEL
DUKTA-MALEN, SYLVIE
MOLINAS, CATHERINE
COURVALIN, PATRICE

ENTERED

(ii) TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
(B) STREET: 1755 S. Jefferson Davis Highway, Suite 400
(C) CITY: Arlington
(D) STATE: Virginia
(E) COUNTRY: U.S.A.
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/357,375
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/286,819
(B) FILING DATE: 05-AUG-1994

(A) APPLICATION NUMBER: US 08/174,682
(B) FILING DATE: 28-DEC-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/917,146

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,375DATE: 05/12/2000
TIME: 14:24:30

INPUT SET: S35473.raw

47 (B) FILING DATE: 10-AUG-1992
48
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: PCT/FR/91/00855
52 (B) FILING DATE: 29-OCT-1991
53
54 (vii) PRIOR APPLICATION DATA:
55 (A) APPLICATION NUMBER: FR 9013579
56 (B) FILING DATE: 31-OCT-1990
57
58
59 (viii) ATTORNEY/AGENT INFORMATION:
60 (A) NAME: Oblon, Norman F.
61 (B) REGISTRATION NUMBER: 24,618
62 (C) REFERENCE/DOCKET NUMBER: 660-060-0 PCT
63
64 (ix) TELECOMMUNICATION INFORMATION:
65 (A) TELEPHONE: (703) 413-3000
66 (B) TELEFAX: (703) 413-2220
67 (C) TELEX: 248855 OPAT UR
68
69 (2) INFORMATION FOR SEQ ID NO:1:
70
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 966 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: unknown
75 (D) TOPOLOGY: linear
76
77 (ii) MOLECULE TYPE: DNA (genomic)
78
79
80 (ix) FEATURE:
81 (A) NAME/KEY: CDS
82 (B) LOCATION: 1..966
83
84
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
86
87 ATG AAT AAC ATC GGC ATT ACT GTT TAT GGA TGT GAG CAG GAT GAG GCA 48
88 Met Asn Asn Ile Gly Ile Thr Val Tyr Gly Cys Glu Gln Asp Glu Ala
89 1 5 10 15
90
91 GAT GCA TTC CAT GCT CTT TCG CCT CGC TTT GGC GTT ATG GCA ACG ATA 96
92 Asp Ala Phe His Ala Leu Ser Pro Arg Phe Gly Val Met Ala Thr Ile
93 20 25 30
94
95 ATT AAC GCC AAC GTG TCG GAA TCC AAC GCC AAA TCC GCG CCT TTC AAT 144
96 Ile Asn Ala Asn Val Ser Glu Ser Asn Ala Lys Ser Ala Pro Phe Asn
97 35 40 45
98
99 CAA TGT ATC AGT GTG GGA CAT AAA TCA GAG ATT TCC GCC TCT ATT CTT 192

RAW SEQUENCE LISTING PATENT APPLICATION US/09/357,375

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TIME: 14:24:30

INPUT SET: S35473.raw

| | | |
|-----|---|-----|
| 100 | Gln Cys Ile Ser Val Gly His Lys Ser Glu Ile Ser Ala Ser Ile Leu | |
| 101 | 50 55 60 | |
| 102 | | |
| 103 | CTT GCG CTG AAG AGA GCC GGT GTG AAA TAT ATT TCT ACC CGA AGC ATC | 240 |
| 104 | Leu Ala Leu Lys Arg Ala Gly Val Lys Tyr Ile Ser Thr Arg Ser Ile | |
| 105 | 65 70 75 80 | |
| 106 | | |
| 107 | GGC TGC AAT CAT ATA GAT ACA ACT GCT GCT AAG AGA ATG GGC ATC ACT | 288 |
| 108 | Gly Cys Asn His Ile Asp Thr Thr Ala Ala Lys Arg Met Gly Ile Thr | |
| 109 | 85 90 95 | |
| 110 | | |
| 111 | GTC GAC AAT GTG GCG TAC TCG CCG GAT AGC GTT GCC GAT TAT ACT ATG | 336 |
| 112 | Val Asp Asn Val Ala Tyr Ser Pro Asp Ser Val Ala Asp Tyr Thr Met | |
| 113 | 100 105 110 | |
| 114 | | |
| 115 | ATG CTA ATT CTT ATG GCA GTA CGC AAC GTA AAA TCG ATT GTG CGC TCT | 384 |
| 116 | Met Leu Ile Leu Met Ala Val Arg Asn Val Lys Ser Ile Val Arg Ser | |
| 117 | 115 120 125 | |
| 118 | | |
| 119 | GTG GAA AAA CAT GAT TTC AGG TTG GAC AGC GAC CGT GGC AAG GTA CTC | 432 |
| 120 | Val Glu Lys His Asp Phe Arg Leu Asp Ser Asp Arg Gly Lys Val Leu | |
| 121 | 130 135 140 | |
| 122 | | |
| 123 | AGC GAC ATG ACA GTT GGT GTG GTG GGA ACG GGC CAG ATA GGC AAA GCG | 480 |
| 124 | Ser Asp Met Thr Val Gly Val Val Gly Thr Gly Gln Ile Gly Lys Ala | |
| 125 | 145 150 155 160 | |
| 126 | | |
| 127 | GTT ATT GAG CGG CTG CGA GGA TTT GGA TGT AAA GTG TTG GCT TAT AGT | 528 |
| 128 | Val Ile Glu Arg Leu Arg Gly Phe Gly Cys Lys Val Leu Ala Tyr Ser | |
| 129 | 165 170 175 | |
| 130 | | |
| 131 | CGC AGC CGA AGT ATA GAG GTA AAC TAT GTA CCG TTT GAT GAG TTG CTG | 576 |
| 132 | Arg Ser Arg Ser Ile Glu Val Asn Tyr Val Pro Phe Asp Glu Leu Leu | |
| 133 | 180 185 190 | |
| 134 | | |
| 135 | CAA AAT AGC GAT ATC GTT ACG CTT CAT GTG CCG CTC AAT ACG GAT ACG | 624 |
| 136 | Gln Asn Ser Asp Ile Val Thr Leu His Val Pro Leu Asn Thr Asp Thr | |
| 137 | 195 200 205 | |
| 138 | | |
| 139 | CAC TAT ATT ATC AGC CAC GAA CAA ATA CAG AGA ATG AAG CAA GGA GCA | 672 |
| 140 | His Tyr Ile Ile Ser His Glu Gln Ile Gln Arg Met Lys Gln Gly Ala | |
| 141 | 210 215 220 | |
| 142 | | |
| 143 | TTT CTT ATC AAT ACT GGG CGC GGT CCA CTT GTA GAT ACC TAT GAG TTG | 720 |
| 144 | Phe Leu Ile Asn Thr Gly Arg Gly Pro Leu Val Asp Thr Tyr Glu Leu | |
| 145 | 225 230 235 240 | |
| 146 | | |
| 147 | GTT AAA GCA TTA GAA AAC GGG AAA CTG GGC GGT GCC GCA TTG GAT GTA | 768 |
| 148 | Val Lys Ala Leu Glu Asn Gly Lys Leu Gly Gly Ala Ala Leu Asp Val | |
| 149 | 245 250 255 | |
| 150 | | |
| 151 | TTG GAA GGA GAG GAA GAG TTT TTC TAC TCT GAT TGC ACC CAA AAA CCA | 816 |
| 152 | Leu Glu Gly Glu Glu Glu Phe Phe Tyr Ser Asp Cys Thr Gln Lys Pro | |

RAW SEQUENCE LISTING PATENT APPLICATION US/09/357,375

DATE: 05/12/2000
TIME: 14:24:31

INPUT SET: S35473.raw

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153          260          265          270
154
155  ATT GAT AAT CAA TTT TTA CTT AAA CTT CAA AGA ATG CCT AAC GTG ATA      864
156  Ile Asp Asn Gln Phe Leu Leu Lys Leu Gln Arg Met Pro Asn Val Ile
157          275          280          285
158
159  ATC ACA CCG CAT ACG GCC TAT TAT ACC GAG CAA GCG TTG CGT GAT ACC      912
160  Ile Thr Pro His Thr Ala Tyr Tyr Thr Glu Gln Ala Leu Arg Asp Thr
161          290          295          300
162
163  GTT GAA AAA ACC ATT AAA AAC TGT TTG GAT TTT GAA AGG AGA CAG GAG      960
164  Val Glu Lys Thr Ile Lys Asn Cys Leu Asp Phe Glu Arg Arg Gln Glu
165  305          310          315          320
166
167  CAT GAA      966
168  His Glu
169
170
171
172  (2) INFORMATION FOR SEQ ID NO:2:
173
174      (i) SEQUENCE CHARACTERISTICS:
175          (A) LENGTH: 322 amino acids
176          (B) TYPE: amino acid
177          (D) TOPOLOGY: linear
178
179      (ii) MOLECULE TYPE: protein
180
181      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
182
183  Met Asn Asn Ile Gly Ile Thr Val Tyr Gly Cys Glu Gln Asp Glu Ala
184      1          5          10          15
185
186  Asp Ala Phe His Ala Leu Ser Pro Arg Phe Gly Val Met Ala Thr Ile
187          20          25          30
188
189  Ile Asn Ala Asn Val Ser Glu Ser Asn Ala Lys Ser Ala Pro Phe Asn
190          35          40          45
191
192  Gln Cys Ile Ser Val Gly His Lys Ser Glu Ile Ser Ala Ser Ile Leu
193          50          55          60
194
195  Leu Ala Leu Lys Arg Ala Gly Val Lys Tyr Ile Ser Thr Arg Ser Ile
196          65          70          75          80
197
198  Gly Cys Asn His Ile Asp Thr Thr Ala Ala Lys Arg Met Gly Ile Thr
199          85          90          95
200
201  Val Asp Asn Val Ala Tyr Ser Pro Asp Ser Val Ala Asp Tyr Thr Met
202          100          105          110
203
204  Met Leu Ile Leu Met Ala Val Arg Asn Val Lys Ser Ile Val Arg Ser
205          115          120          125

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PATENT APPLICATION US/09/357,375DATE: 05/12/2000
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INPUT SET: S35473.raw

206
207 Val Glu Lys His Asp Phe Arg Leu Asp Ser Asp Arg Gly Lys Val Leu
208 130 135 140
209
210 Ser Asp Met Thr Val Gly Val Val Gly Thr Gly Gln Ile Gly Lys Ala
211 145 150 155 160
212
213 Val Ile Glu Arg Leu Arg Gly Phe Gly Cys Lys Val Leu Ala Tyr Ser
214 165 170 175
215
216 Arg Ser Arg Ser Ile Glu Val Asn Tyr Val Pro Phe Asp Glu Leu Leu
217 180 185 190
218
219 Gln Asn Ser Asp Ile Val Thr Leu His Val Pro Leu Asn Thr Asp Thr
220 195 200 205
221
222 His Tyr Ile Ile Ser His Glu Gln Ile Gln Arg Met Lys Gln Gly Ala
223 210 215 220
224
225 Phe Leu Ile Asn Thr Gly Arg Gly Pro Leu Val Asp Thr Tyr Glu Leu
226 225 230 235 240
227
228 Val Lys Ala Leu Glu Asn Gly Lys Leu Gly Gly Ala Ala Leu Asp Val
229 245 250 255
230
231 Leu Glu Gly Glu Glu Glu Phe Phe Tyr Ser Asp Cys Thr Gln Lys Pro
232 260 265 270
233
234 Ile Asp Asn Gln Phe Leu Leu Lys Leu Gln Arg Met Pro Asn Val Ile
235 275 280 285
236
237 Ile Thr Pro His Thr Ala Tyr Tyr Thr Glu Gln Ala Leu Arg Asp Thr
238 290 295 300
239
240 Val Glu Lys Thr Ile Lys Asn Cys Leu Asp Phe Glu Arg Arg Gln Glu
241 305 310 315 320
242
243 His Glu
244
245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/357,375

DATE: 05/12/2000
TIME: 14:24:31

INPUT SET: S35473.raw

Line

Error

Original Text